

-106-

- (2) INFORMATION FOR SEQ ID NO:7:
- (1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 709 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Homo sapiens
- (vii) IMMEDIATE SOURCE:  
 (B) CLONE: alpha-hemoglobin
- (ix) FEATURE:  
 (A) NAME/KEY: transit\_peptide (B) LOCATION:  
 26..241  
 (B) LOCATION: 26..241
- (ix) FEATURE:  
 (A) NAME/KEY: CDS  
 (B) LOCATION: 245..670
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

CTGAGGGCA TCTGATCTTT CAAGAATGGC ACAAATTAAC AACATGGCAC  
AAGGGATACA 60

AACCCTTAAT CCCAATTCCA ATTTCCATAA ACCCCAAGTT CCTAAATCTT  
CAAGTTTCT 120

TGTTTTTGA TGTAAAAAC TGAATTC AGCAAATTCT ATGTTGGTTT TGAAAAA  
TTCAATTTT ATGCAAAAGT TTTGTTCTT TAGGATTTC GCAGGTGGTA 240

GAGTTTCTTG 240

CATG GTG CTG TCT CCT GCC GAC AAG ACC AAC GTC AAG GCC GCC TGG GGC  
289

Val Leu Ser Pro Ala Asp Lys Thr Asn Val Lys Ala Ala Trp Gly  
1 5 10 15

AAG CTT GCG GCG CAC GCT GGC GAG TAT GGT GCG GAG GCC CTG GAG AGG 37

Lys Val Gly Ala His Ala Gly Glu Tyr Gly Ala Glu Ala Leu Glu Arg  
20 25 30

-107-

ATG TTC CTG TCC TTC CCC ACC ACC AAG ACC TAC TTC CCG CAC TTC GAG 35  
 Met Phe Leu Ser Phe Pro Thr Thr Lys Thr Tyr Phe Pro His Phe Asp 40 45  
 CTG AGC CAC GGC TCT GCC CAG GTT AAG GGC CAC GGC AAG AAG GTG GAG 50 55 60  
 Leu Ser His Gly Ser Ala Gln Val Lys Gly His Gly Lys Lys Val Ala 65  
 GAC GCG CTG ACC AAC GCC GTG GCG CAC GTG GAC GAC ATG CCC AAC GAG 70 75  
 Asp Ala Leu Thr Asn Ala Val Ala His Val Asp Asp Met Pro Asn Ala 80  
 CTG TCC GCC CTG AGC GAC CTG CAC GCG CAC AAG CTT CCG GTG GAC CAG 85 90 95  
 Leu Ser Ala Leu Ser Asp Leu His Ala His Lys Leu Arg Val Asp Pro 100  
 GTC AAC TTC AAG CTC CTA AGC CAC TGC CTG CTG GTG ACC CTG GCC GAG 105 110  
 Val Asn Phe Lys Leu Leu Ser His Cys Leu Leu Val Thr Leu Ala Ala 115  
 CAC CTC CCC GCC GAG TTC ACC CCT GCG GTG CAC GCC TCC CTG GAC AAG 120 125  
 His Leu Pro Ala Glu Phe Thr Pro Ala Val His Ala Ser Leu Asp Lys 130  
 TTC CTG GCT TCT GTG AGC ACC CTG CTG ACC TCC AAA TAC CGT 135 140  
 TAAGCTGGAG  
 Phe Leu Ala Ser Val Ser Thr Val Leu Thr Ser Lys Tyr Arg 140  
 CCTCGGTAGC CGTTCCTCCT GCCCGGTCCA CC

677

- (2) INFORMATION FOR SEQ ID NO:8:
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 141 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (ix) SEQUENCE DESCRIPTION: SEQ ID NO:8:

-108-

Val Leu Ser Pro Ala Asp Lys Thr Asn Val Lys Ala Ala Trp Gly Lys  
 1 5 10 15  
 Val Gly Ala His Ala Gly Glu Tyr Gly Ala Glu Ala Leu Glu Arg Met  
 20 25 30  
 Phe Leu Ser Phe Pro Thr Thr Lys Thr Tyr Phe Pro His Phe Asp Leu  
 35 40 45  
 Ser His Gly Ser Ala Gln Val Lys Gly His Gly Lys Lys Val Ala Asp  
 50 55 60  
 Ala Leu Thr Asn Ala Val Ala His Val Asp Asp Met Pro Asn Ala Leu  
 65 70 75 80  
 Ser Ala Leu Ser Asp Leu His Ala His Lys Leu Arg Val Asp Pro Val  
 85 90 95  
 Asn Phe Lys Leu Leu Ser His Cys Leu Leu Val Thr Leu Ala Ala His  
 100 105 110  
 Leu Pro Ala Glu Phe Thr Pro Ala Val His Ala Ser Leu Asp Lys Phe  
 115 120 125  
 Leu Ala Ser Val Ser Thr Val Leu Thr Ser Lys Tyr Arg  
 130 135 140

## (2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 743 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) ORIGINAL SOURCE:
  - (A) ORGANISM: Homo sapiens
- (vii) IMMEDIATE SOURCE:
  - (B) CLONE: beta-hemoglobin
- (ix) FEATURE:
  - (A) NAME/KEY: transit\_peptide (B) LOCATION: 26..241

-109-

(B) LOCATION: 26..241

(ix)

FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 245..685

(xi)

SEQUENCE DESCRIPTION: SEQ ID NO: 9:

CTCGAGGGGA TCTGATCTTT CAAGAATGGC ACAAATTAAC AACATGGCAC 60  
AAGGGATACA

AACCCTTAAT CCCAATTCCA ATTTCCATAA ACCCCAAGTT CCTAAATCTT 120  
CAAGTTTCT

TGTTTTTGA TCTAAAAAC TGAAAAATTC AGCAAATTCT ATGTTGGTTT 180  
TGAAAAAGA

TTCAATTTT ATGCAAAAGT TTTGTCCTT TAGGATTCA GCAGGTGTA 240  
GAGTTTCTTG

GATG GTG CAC CTG ACT CCT GAG GAG AAG TCT GCC GTT ACT GCC CTG TGG 289  
Val His Leu Thr Pro Glu Glu Lys Ser Ala Val Thr Ala Leu Trp  
1 5 10 15

GGC AAG GTG AAC GTG GAT GAA GTT GCT GGT GAG GCC CTG GGC AGG CTT 30  
Gly Lys Val Asn Val Asp Glu Val Gly Gly Glu Ala Leu Gly Arg Leu  
20 25 30

CTG GTG GTC TAC CCT TGG ACC CAG AGG TTC TTT GAG TCC TTT GGC GAG 35  
Leu Val Val Tyr Pro Trp Thr Gln Arg Phe Phe Glu Ser Phe Gly Asp  
35 40 45

CTG TCC ACT CCT GAT GCT GTT ATG GGC AAC CCT AAG GTG AAG GCT CAG 40  
Leu Ser Thr Pro Asp Ala Val Met Gly Asn Pro Lys Val Lys Ala His  
50 55 60

GGC AAG AAA GTG CTG GGT GCC TTT AGT GAT GGC CTG GCT CAC CTG GAG 45  
Gly Lys Lys Val Leu Gly Ala Phe Ser Asp Gly Leu Ala His Leu Asp  
65 70 75

AAC CTC AAG GGC ACC TTT GCC ACCA CTC AGT GAG CTG CAC TGT GAC AAG 50  
Asn Leu Lys Gly Thr Phe Ala Thr Leu Ser Glu Leu His Cys Asp Lys  
80 85 90 95

-110-

CTG CAC GTG GAT CCT GAG AGC TTC AGG CTC CTA GGC AAC GTG CTG GTC 7  
Leu His Val Asp Pro Glu Ser Phe Arg Leu Leu Gly Asn Val Leu Val  
100 105 110  
TGT GTG CTG GCG CAT CAC TTT GGC AAA GAA TTC ACC CCA CCA GTG CAC 25  
Cys Val Leu Ala His His Phe Gly Lys Glu Phe Thr Pro Pro Val Gln  
115 120 125  
GCT GCC TAT CAG AAA GTG GTG GCT GGT CTG GCT AAT GCC CTG GCC CAC 3  
Ala Ala Tyr Gln Lys Val Val Ala Gly Val Ala Asn Ala Leu Ala His  
130 135 140  
AAG TAT CAC TAAGCTCGCT TTCTTGCTGT CCAATTCTA TTAAAGGTTT 722  
Lys Tyr His  
145  
CITTGTGGGG TCGAGGTCCA C 743

- (2) INFORMATION FOR SEQ ID NO: 10:
- (1) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 146 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:
- Val His Leu Thr Pro Glu Glu Lys Ser Ala Val Thr Ala Leu Trp Gly  
1 5 10 15  
Lys Val Asn Val Asp Glu Val Gly Gly Glu Ala Leu Gly Arg Leu Leu  
20 25 30  
Val Val Tyr Pro Trp Thr Gln Arg Phe Phe Glu Ser Phe Gly Asp Leu  
35 40 45  
Ser Thr Pro Asp Ala Val Met Gly Asn Pro Lys Val Lys Ala His Gly  
50 55 60  
Lys Lys Val Leu Gly Ala Phe Ser Asp Gly Leu Ala His Leu Asp Asn  
65 70 75 80  
Leu Lys Gly Thr Phe Ala Thr Leu Ser Glu Leu His Cys Asp Lys Leu  
85 90 95